

SEQUENCE LISTING

<110> AnGes MG, Inc.

<120> Medicine to impediment to auditory functioning

<130> 03059PCT

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 728

<212> PRT

<213> Homo Sapiens

<400> 1

```

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
  1             5             10             15
Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
             20             25             30
Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
             35             40             45
Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
             50             55             60
Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
             65             70             75             80
Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
             85             90             95
Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
             100            105            110
Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
             115            120            125
Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
             130            135            140
Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
             145            150            155            160
Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
             165            170            175
Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser
             180            185            190
Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
             195            200            205

```

Val	Glu	Cys	Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Leu	Met	Asp	210	215	220	
His	Thr	Glu	Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	Gln	Thr	Pro	225	230	235	240
His	Arg	His	Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	Gly	Phe	Asp	245	250	255	
Asp	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	Trp	Cys	Tyr	260	265	270	
Thr	Leu	Asp	Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	Lys	Thr	Cys	275	280	285	
Ala	Asp	Asn	Thr	Met	Asn	Asp	Thr	Asp	Val	Pro	Leu	Glu	Thr	Thr	Glu	290	295	300	
Cys	Ile	Gln	Gly	Gln	Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Val	Asn	Thr	Ile	305	310	315	320
Trp	Asn	Gly	Ile	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Tyr	Pro	His	Glu	325	330	335	
His	Asp	Met	Thr	Pro	Glu	Asn	Phe	Lys	Cys	Lys	Asp	Leu	Arg	Glu	Asn	340	345	350	
Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ser	Pro	Trp	Cys	Phe	Thr	Thr	355	360	365	
Asp	Pro	Asn	Ile	Arg	Val	Gly	Tyr	Cys	Ser	Gln	Ile	Pro	Asn	Cys	Asp	370	375	380	
Met	Ser	His	Gly	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Lys	Asn	Tyr	Met	385	390	395	400
Gly	Asn	Leu	Ser	Gln	Thr	Arg	Ser	Gly	Leu	Thr	Cys	Ser	Met	Trp	Asp	405	410	415	
Lys	Asn	Met	Glu	Asp	Leu	His	Arg	His	Ile	Phe	Trp	Glu	Pro	Asp	Ala	420	425	430	
Ser	Lys	Leu	Asn	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asp	Asp	Ala	His	435	440	445	
Gly	Pro	Trp	Cys	Tyr	Thr	Gly	Asn	Pro	Leu	Ile	Pro	Trp	Asp	Tyr	Cys	450	455	460	
Pro	Ile	Ser	Arg	Cys	Glu	Gly	Asp	Thr	Thr	Pro	Thr	Ile	Val	Asn	Leu	465	470	475	480
Asp	His	Pro	Val	Ile	Ser	Cys	Ala	Lys	Thr	Lys	Gln	Leu	Arg	Val	Val	485	490	495	
Asn	Gly	Ile	Pro	Thr	Arg	Thr	Asn	Ile	Gly	Trp	Met	Val	Ser	Leu	Arg	500	505	510	
Tyr	Arg	Asn	Lys	His	Ile	Cys	Gly	Gly	Ser	Leu	Ile	Lys	Glu	Ser	Trp	515	520	525	

Val	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Pro	Ser	Arg	Asp	Leu	Lys	Asp	Tyr
530						535					540				
Glu	Ala	Trp	Leu	Gly	Ile	His	Asp	Val	His	Gly	Arg	Gly	Asp	Glu	Lys
545					550					555					560
Cys	Lys	Gln	Val	Leu	Asn	Val	Ser	Gln	Leu	Val	Tyr	Gly	Pro	Glu	Gly
			565						570					575	
Ser	Asp	Leu	Val	Leu	Met	Lys	Leu	Ala	Arg	Pro	Ala	Val	Leu	Asp	Asp
		580						585					590		
Phe	Val	Ser	Thr	Ile	Asp	Leu	Pro	Asn	Tyr	Gly	Cys	Thr	Ile	Pro	Glu
	595					600					605				
Lys	Thr	Ser	Cys	Ser	Val	Tyr	Gly	Trp	Gly	Tyr	Thr	Gly	Leu	Ile	Asn
610						615					620				
Tyr	Asp	Gly	Leu	Leu	Arg	Val	Ala	His	Leu	Tyr	Ile	Met	Gly	Asn	Glu
625					630					635					640
Lys	Cys	Ser	Gln	His	His	Arg	Gly	Lys	Val	Thr	Leu	Asn	Glu	Ser	Glu
			645						650				655		
Ile	Cys	Ala	Gly	Ala	Glu	Lys	Ile	Gly	Ser	Gly	Pro	Cys	Glu	Gly	Asp
		660						665					670		
Tyr	Gly	Gly	Pro	Leu	Val	Cys	Glu	Gln	His	Lys	Met	Arg	Met	Val	Leu
	675						680					685			
Gly	Val	Ile	Val	Pro	Gly	Arg	Gly	Cys	Ala	Ile	Pro	Asn	Arg	Pro	Gly
690						695					700				
Ile	Phe	Val	Arg	Val	Ala	Tyr	Tyr	Ala	Lys	Trp	Ile	His	Lys	Ile	Ile
705					710					715					720
Leu	Thr	Tyr	Lys	Val	Pro	Gln	Ser								
							725								

<210> 2

<211> 2187

<212> DNA

<213> Homo Sapiens

<400> 2

```

atgtgggtga ccaaactcct gccagccctg ctgctgcagc atgtcctcct gcattctcctc 60
ctgctcccca tcgccatccc ctatgcagag ggacaaagga aaagaagaaa tacaattcat 120
gaattcaaaa aatcagcaaa gactacccta atcaaaatag atccagcact gaagataaaa 180
acaaaaaag tgaatactgc agaccaatgt gctaatagat gtactaggaa taaaggactt 240
ccattcactt gcaaggcttt tgtttttgat aaagcaagaa aacaatgcct ctggttcccc 300
ttcaatagca tgtcaagtgg agtgaaaaaa gaatttggcc atgaatttga cctctatgaa 360
aacaaagact acattagaaa ctgcatcatt ggtaaaggac gcagctacaa gggaacagta 420

```

```

tctatcacta agagtggcat caaatgtcag ccctggagtt ccatgatacc acacgaacac 480
agctttttgc cttcgagcta tcggggtaaa gacctacagg aaaactactg tcgaaatcct 540
cgaggggaag aagggggacc ctggtgtttc acaagcaatc cagaggtacg ctacgaagtc 600
tgtgacattc ctcagtgttc agaagttgaa tgcattgacct gcaatgggga gagttatcga 660
ggtctcatgg atcatacaga atcaggcaag atttgtcagc gctgggatca tcagacacca 720
caccggcaca aattcttgcc tgaaagatat cccgacaagg gctttgatga taattattgc 780
cgcaatcccg atggccagcc gaggccatgg tgctatactc ttgaccctca caccgcctgg 840
gagtactgtg caattaaaac atgcgctgac aatactatga atgacactga tgttcctttg 900
gaaacaactg aatgcatcca aggtcaagga gaaggctaca ggggcactgt caataccatt 960
tggaatggaa ttccatgtca gcgttgggat tctcagtatc ctcacgagca tgacatgact 1020
cctgaaaatt tcaagtgcaa ggacctacga gaaaattact gccgaaatcc agatgggtct 1080
gaatcaccct ggtgttttac cactgatcca aacatccgag ttggctactg ctcccaaatt 1140
ccaaactgtg atatgtcaca tggacaagat tgttatcgtg ggaatggcaa aaattatatg 1200
ggcaacttat cccaaacaag atctggacta acatgttcaa tgtgggacaa gaacatggaa 1260
gacttacatc gtcatatctt ctgggaacca gatgcaagta agctgaatga gaattactgc 1320
cgaaatccag atgatgatgc tcatggaccc tgggtgctaca cgggaaatcc actcattcct 1380
tgggattatt gccctatttc tcgttgtgaa ggtgatacca cacctacaat agtcaattta 1440
gaccatcccc taatatcttg tgccaaaacg aaacaattgc gagttgtaaa tgggattcca 1500
acacgaacaa acataggatg gatgggttagt ttgagataca gaaataaaca tatctgcgga 1560
ggatcattga taaaggagag ttgggttctt actgcacgac agtgtttccc ttctcgagac 1620
ttgaaagatt atgaagcttg gcttgggaatt catgatgtcc acggaagagg agatgagaaa 1680
tgcaaacagg ttctcaatgt ttcccagctg gtatatggcc ctgaaggatc agatctggtt 1740
ttaatgaagc ttgccaggcc tgctgtcctg gatgattttg ttagtacgat tgatttacct 1800
aattatggat gcacaattcc tgaaaagacc agttgcagtg tttatggctg gggctacact 1860
ggattgatca actatgatgg cctattacga gtggcacatc tctatataat gggaaatgag 1920
aaatgcagcc agcatcatcg agggaagggt actctgaatg agtctgaaat atgtgctggg 1980
gctgaaaaga ttggatcagg accatgtgag ggggattatg gtggcccact tgtttgtgag 2040
caacataaaa tgagaatggt tcttggtgtc attgttcctg gtcgtggatg tgccattcca 2100
aatcgtcctg gtatttttgt ccgagtagca tattatgcaa aatggataca caaaattatt 2160
ttaacatata aggtaccaca gtcatag
2187

```

<210> 3

<211> 24

<212> DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence Synthetic DNA

<400> 3

TTCACAAGCA ATCCAGAGGT ACGC

20

<210> 4
<211> 24
<212> DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence Synthetic
DNA
<400> 4
GAGGGTCAAG AGTATAGCAC CATG

20

<210> 5
<211> 20
<212> DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence Synthetic
DNA
<400> 5
TGAAGGTCGG AGTCAACGGA

20

<210> 6
<211> 20
<212> DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence Synthetic
DNA
<400> 6
GATGGCATGG ACTGTGGTCA

20